

178363

STIC-Biotech/ChemLib

From: Chernyshev, Olga
Sent: Wednesday, February 01, 2006 2:20 PM
To: STIC-Biotech/ChemLib
Subject: 10/815,297, sequence search request

Please search SEQ ID NO: 3 down to 60% identity in regular databases only.
Thank you very much!

Olga N. Chernyshev, Ph.D.
AU 1649
REM 3C89
2-0870
mail 4C70

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FEB - 1 2006
STIC-BIOTECH

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 7, 2006, 20:47:32 ; Search time 17 Seconds
(without alignment)
375.667 Million cell updates/sec

Title: US-10-815-297-3
Perfect score: 2872
Sequence: 1 MLKQSERRRSWSYRPMWTTT.....KKIAECLGSPQLTPROEN 545

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 60%
Maximum Match 100%
Listing first 500 summaries

Database :

Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubpa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUB.pep:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| ----- | | | | | |

No matches found

Search completed: February 7, 2006, 20:50:43
Job time : 17 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 7, 2006, 20:46:31 ; Search time 180 seconds
(without alignments)
1265.094 Million cell updates/sec

Title: US-10-815-297-3
Perfect score: 2872
Sequence: 1 MLKOSERRSRWSYRPMNTTE.....KKIAECLGSPNQLTPROEN 545

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%
Maximum Match 100%
Listing first 500 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------------|---------------------|
| 1 | 2872 | 100.0 | 545 | US-09-918-359-2 | Sequence 2, Appl1 |
| 2 | 2872 | 100.0 | 545 | US-09-833-466-3 | Sequence 3, Appl1 |
| 3 | 2872 | 100.0 | 545 | US-10-815-297-3 | Sequence 36, Appl1 |
| 4 | 2862 | 99.7 | 545 | US-09-999-2208-16 | Sequence 116, Appl1 |
| 5 | 2862 | 99.7 | 545 | US-09-999-2208-116 | Sequence 120, Appl1 |
| 6 | 2857 | 99.5 | 545 | US-09-999-2208-120 | Sequence 2, Appl1 |
| 7 | 2849 | 99.2 | 545 | US-09-999-2208-2 | Sequence 24, Appl1 |
| 8 | 2803.5 | 97.6 | 545 | US-10-380-727-24 | Sequence 34, Appl1 |
| 9 | 2781 | 96.8 | 545 | US-09-999-2208-34 | Sequence 118, Appl1 |
| 10 | 2778 | 96.7 | 545 | US-09-999-2208-118 | Sequence 44, Appl1 |
| 11 | 2401 | 83.6 | 467 | US-10-114-270-44 | |

ALIGNMENTS

RESULT 1
US-09-918-359-2
; Sequence 2, Application US/09/83359
; Publication No. US2003006449A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Made
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Gerhardt, Brenda
; TITLE OF INVENTION: Novel Human Ion Channel Proteins and Polynucleotides Encoding the

;; TITLE OF INVENTION: Same
;; FILE REFERENCE: LEX-0208-USA
;; CURRENT APPLICATION NUMBER: US/09/918,359
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: US 60/221,643
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: US 60/222,503
;; PRIOR FILING DATE: 2000-08-02
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 545
;; TYPE: PRT
;; ORGANISM: homo sapiens
US-09-918-359-2

Query Match 100.0%; Score 2872; DB 3; Length 545;
Best Local Similarity 100.0%; Pred. No. 5.9e-265;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MLKOSERRSRWSYRPMNTTENEGSHRSICIGARSQSQASIHGMTEGNNVYIIEBDD | 60 |
| DB | 1 | MLKOSERRSRWSYRPMNTTENEGSHRSICIGARSQSQASIHGMTEGNNVYIIEBDD | 60 |
| QY | 61 | GEEDQWKDLDLEDDQAGEVTTAKPEGSDPPALSTLNANVGGHSYOLDYCELAGFPK | 120 |
| DB | 61 | GEEDQWKDLDLEDDQAGEVTTAKPEGSDPPALSTLNANVGGHSYOLDYCELAGFPK | 120 |
| QY | 121 | TLGLRLATSTSRSLCDDYEEQTDYFDRDPAVPOLYNPFYLSGLVLDGICPRR | 180 |
| DB | 121 | TLGLRLATSTSRSLCDDYEEQTDYFDRDPAVPOLYNPFYLSGLVLDGICPRR | 180 |
| QY | 181 | PLIEELGVGVKRYKTPRCRCICEERRDELSPRLKIOHELRQAOVEAEELPRMRFGY | 240 |
| DB | 181 | PLIEELGVGVKRYKTPRCRCICEERRDELSPRLKIOHELRQAOVEAEELPRMRFGY | 240 |
| QY | 241 | PORRLMLMEKPFSSVAKAIGVASTFVLVVALANTVEEMQOHSOGEGGPDLP | 300 |
| DB | 241 | PORRLMLMEKPFSSVAKAIGVASTFVLVVALANTVEEMQOHSOGEGGPDLP | 300 |
| QY | 301 | ILIEHEVMLCMGFTELYLRLASTPDRLRRFARSALNLDVLAIPLYQLLIECTGEGH | 360 |
| DB | 301 | ILIEHEVMLCMGFTELYLRLASTPDRLRRFARSALNLDVLAIPLYQLLIECTGEGH | 360 |
| QY | 361 | QRGQTVGSVKGQVLRVWRMRIRILKLABSHSGLAFFGTLRQCVQOVGCLLFTIM | 420 |
| DB | 361 | QRGQTVGSVKGQVLRVWRMRIRILKLABSHSGLAFFGTLRQCVQOVGCLLFTIM | 420 |
| QY | 421 | GIFTSAAYVSEHVPSTNFTTIPHSMMMAVSIISVGYGDMYDETHLGRFAFLCIAF | 480 |
| DB | 421 | GIFTSAAYVSEHVPSTNFTTIPHSMMMAVSIISVGYGDMYDETHLGRFAFLCIAF | 480 |
| QY | 481 | GIILGMPISILYNKFSVDYSKLKAYEYTTIRERGEVNFQRAKKIACLLGSPQLT | 540 |
| DB | 481 | GIILGMPISILYNKFSVDYSKLKAYEYTTIRERGEVNFQRAKKIACLLGSPQLT | 540 |
| QY | 541 | PROEN 545 | |
| DB | 541 | PROEN 545 | |

RESULT 2
US-09-833-466-3
; Sequence 3, Application US/09/833466
; Publication No. US2004005357A1
; GENERAL INFORMATION:
; APPLICANT: Jegalet, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: Kv10.1, a No. US2004005357A1el Voltage-Gated Potassium Channel F
; FILE REFERENCE: 018512-005910US
; CURRENT APPLICATION NUMBER: US/09/833,466
; CURRENT FILING DATE: 2001-04-11

```
/ PRIOR APPLICATION NUMBER: US 60/197,793
/ PRIOR FILING DATE: 2000-04-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 545
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human alpha subunit of voltage-gated potassium
/ FEATURE:
/ OTHER INFORMATION: channel Kv10.1
/ NAME/KEY: PEPTIDE
/ LOCATION: (102)..(514)
/ OTHER INFORMATION: conserved region of voltage-gated potassium
/ OTHER INFORMATION: channel Kv10.1
US-09-833-466-3

Query Match      100.0%; Score 2872; DB 3; Length 545;
Best Local Similarity 100.0%; Pred. No. 5,9e-265;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLKQSRRRSWSYRPMNTTNEGSHRRSICSLGARSQSQASIHGWTGNNVNYIEEDD 60
        |||
        1 MLKQSRRRSWSYRPMNTTNEGSHRRSICSLGARSQSQASIHGWTGNNVNYIEEDD 60
DB
QY      61 GEEEDQMKDLAEEDQAGEVTTAKPEGSDPDPALLSTLNNVNGHSYOLDYCELAGFPK 120
        |||
        61 GEEEDQMKDLAEEDQAGEVTTAKPEGSDPDPALLSTLNNVNGHSYOLDYCELAGFPK 120
DB
QY      121 TRIGRLATSTSRQSLSCDYEEOQDEYFPDPDAVQVLYNFIYLSGVLVLDGLCPRR 180
        |||
        121 TRIGRLATSTSRQSLSCDYEEOQDEYFPDPDAVQVLYNFIYLSGVLVLDGLCPRR 180
DB
QY      181 FLEELGYMGVRLKYTPRCRCICEERRDELSERLKIOHELRAQAVEAEELFRDMRFYG 240
        |||
        181 FLEELGYMGVRLKYTPRCRCICEERRDELSERLKIOHELRAQAVEAEELFRDMRFYG 240
DB
QY      241 PQRRLNLMMEKPFSSVAAKAIGVASTFVLVSVALANTVEEMQOHSQGEGBDLP 300
        |||
        241 PQRRLNLMMEKPFSSVAAKAIGVASTFVLVSVALANTVEEMQOHSQGEGBDLP 300
DB
QY      301 ILEHEVLMCMGFTEYLLRLASTPDLRRPARSALNVDVAIPLYLQLLLECFTEGEGH 360
        |||
        301 ILEHEVLMCMGFTEYLLRLASTPDLRRPARSALNVDVAIPLYLQLLLECFTEGEGH 360
DB
QY      361 ORGQTVGSVGVQVLRVWMLMIFRLIKLARHSTGLRAFGFTLRQCYOQVGCCLLFIAM 420
        |||
        361 ORGQTVGSVGVQVLRVWMLMIFRLIKLARHSTGLRAFGFTLRQCYOQVGCCLLFIAM 420
DB
QY      421 GIPTSSAAVSVSHDVPSTNFTTIPHSWMAAVSISTVGDMYPETHLGRFAFLCIAF 480
        |||
        421 GIPTSSAAVSVSHDVPSTNFTTIPHSWMAAVSISTVGDMYPETHLGRFAFLCIAF 480
DB
QY      481 GIILNMPISILYNKFSDDYYSKLKAYEYTTIRREGEVNFMRARAKKIACCLGSPDLT 540
        |||
        481 GIILNMPISILYNKFSDDYYSKLKAYEYTTIRREGEVNFMRARAKKIACCLGSPDLT 540
DB
QY      541 PROEN 545
        |||
        541 PROEN 545
DB
```

RESULT 3
US-10-815-297-3

```
/ Sequence 3, Application US/10815297-3
/ Publication No. US20040157261A1
/ GENERAL INFORMATION:
/ APPLICANT: Jegla, Timothy James
/ APPLICANT: ICAGEN, Inc.
/ TITLE OF INVENTION: Kv10.1, a Novel Voltage-Gated Potassium Channel From
/ TITLE OF INVENTION: Human Brain
/ FILE REFERENCE: 018512-005910US
```

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/ CURRENT APPLICATION NUMBER: US/10/815,297
/ CURRENT FILING DATE: 2004-03-31
/ PRIOR APPLICATION NUMBER: US/09/833,466
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: US 60/197,793
/ PRIOR FILING DATE: 2000-04-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 545
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human alpha subunit of voltage-gated potassium
/ OTHER INFORMATION: channel Kv10.1
/ NAME/KEY: PEPTIDE
/ LOCATION: (102)..(514)
/ OTHER INFORMATION: conserved region of voltage-gated potassium
/ OTHER INFORMATION: channel Kv10.1
US-10-815-297-3

Query Match      100.0%; Score 2872; DB 4; Length 545;
Best Local Similarity 100.0%; Pred. No. 5,9e-265;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLKQSRRRSWSYRPMNTTNEGSHRRSICSLGARSQSQASIHGWTGNNVNYIEEDD 60
        |||
        1 MLKQSRRRSWSYRPMNTTNEGSHRRSICSLGARSQSQASIHGWTGNNVNYIEEDD 60
DB
QY      61 GEEEDQMKDLAEEDQAGEVTTAKPEGSDPDPALLSTLNNVNGHSYOLDYCELAGFPK 120
        |||
        61 GEEEDQMKDLAEEDQAGEVTTAKPEGSDPDPALLSTLNNVNGHSYOLDYCELAGFPK 120
DB
QY      121 TRIGRLATSTSRQSLSCDYEEOQDEYFPDPDAVQVLYNFIYLSGVLVLDGLCPRR 180
        |||
        121 TRIGRLATSTSRQSLSCDYEEOQDEYFPDPDAVQVLYNFIYLSGVLVLDGLCPRR 180
DB
QY      181 FLEELGYMGVRLKYTPRCRCICEERRDELSERLKIOHELRAQAVEAEELFRDMRFYG 240
        |||
        181 FLEELGYMGVRLKYTPRCRCICEERRDELSERLKIOHELRAQAVEAEELFRDMRFYG 240
DB
QY      241 PQRRLNLMMEKPFSSVAAKAIGVASTFVLVSVALANTVEEMQOHSQGEGBDLP 300
        |||
        241 PQRRLNLMMEKPFSSVAAKAIGVASTFVLVSVALANTVEEMQOHSQGEGBDLP 300
DB
QY      301 ILEHEVLMCMGFTEYLLRLASTPDLRRPARSALNVDVAIPLYLQLLLECFTEGEGH 360
        |||
        301 ILEHEVLMCMGFTEYLLRLASTPDLRRPARSALNVDVAIPLYLQLLLECFTEGEGH 360
DB
QY      361 ORGQTVGSVGVQVLRVWMLMIFRLIKLARHSTGLRAFGFTLRQCYOQVGCCLLFIAM 420
        |||
        361 ORGQTVGSVGVQVLRVWMLMIFRLIKLARHSTGLRAFGFTLRQCYOQVGCCLLFIAM 420
DB
QY      421 GIPTSSAAVSVSHDVPSTNFTTIPHSWMAAVSISTVGDMYPETHLGRFAFLCIAF 480
        |||
        421 GIPTSSAAVSVSHDVPSTNFTTIPHSWMAAVSISTVGDMYPETHLGRFAFLCIAF 480
DB
QY      481 GIILNMPISILYNKFSDDYYSKLKAYEYTTIRREGEVNFMRARAKKIACCLGSPDLT 540
        |||
        481 GIILNMPISILYNKFSDDYYSKLKAYEYTTIRREGEVNFMRARAKKIACCLGSPDLT 540
DB
QY      541 PROEN 545
        |||
        541 PROEN 545
DB
```

RESULT 4
US-09-999-2208-36

```
/ Sequence 36, Application US/099992208
/ Publication No. US20030059923A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 20:45:41 ; Search time 51 Seconds

(without alignments)
883.495 Million cell updates/sec

Title: US-10-815-297-3

Sequence: 1 MLKSERRRSMYSYPMWNTTE.....KKIAECLLSNPOLTPROEN 545

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 60%
Listing first 500 summaries

Database: Issued Patents AA:

1: /cgn2_6/pdata/1/1aa/5_COMB.pep:*
2: /cgn2_6/pdata/1/1aa/6_COMB.pep:*
3: /cgn2_6/pdata/1/1aa/H_COMB.pep:*
4: /cgn2_6/pdata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/pdata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/pdata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------|
| 1 | 2872 | 100.0 | 545 | 2 | US-09-833-466-3 |

ALIGNMENTS

RESULT 1
US-09-833-466-3 Application US/09833466
Patent No. 6727353
GENERAL INFORMATION:
APPLICANT: Jegla, Timothy James
APPLICANT: ICAGEN, Inc.
TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-Gated Potassium Channel From
FILE REFERENCE: 018512-005910US
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 545
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

OTHER INFORMATION: human alpha subunit of voltage-gated potassium
OTHER INFORMATION: channel Kv10.1
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (102)..(514)
OTHER INFORMATION: conserved region of voltage-gated potassium
OTHER INFORMATION: channel Kv10.1
US-09-833-466-3

Query Match 100.0%; Score 2872; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 4.8e-294;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MLKSERRRSMYSYPMWNTTEGSHRSISGLARSGSQASIHGMTEGNNYIIEEDD | 60 |
| DB | 1 | MLKSERRRSMYSYPMWNTTEGSHRSISGLARSGSQASIHGMTEGNNYIIEEDD | 60 |
| QY | 61 | GEEDQWMDLAEBDQAGEVTTAKPEGSPDPALLSTLNVVGGHSYQLDYCELAGFPK | 120 |
| DB | 61 | GEEDQWMDLAEBDQAGEVTTAKPEGSPDPALLSTLNVVGGHSYQLDYCELAGFPK | 120 |
| QY | 121 | TRLGRLATSTRSRQLSLCDYEEQTDYFFDRDPAYVQLYNYFSLGVLVLDGLCPRR | 180 |
| DB | 121 | TRLGRLATSTRSRQLSLCDYEEQTDYFFDRDPAYVQLYNYFSLGVLVLDGLCPRR | 180 |
| QY | 181 | FLEELGYGVRLKTPRCRCRICEERRDELSERLKIOHELPAQAQVEAEELFRDMRFYG | 240 |
| DB | 181 | FLEELGYGVRLKTPRCRCRICEERRDELSERLKIOHELPAQAQVEAEELFRDMRFYG | 240 |
| QY | 241 | PORRLNMLMEKPFSSVAKAIGVASTFVLVSVALALNTVEEMQOHSQGGEGGPDLP | 300 |
| DB | 241 | PORRLNMLMEKPFSSVAKAIGVASTFVLVSVALALNTVEEMQOHSQGGEGGPDLP | 300 |
| QY | 301 | ILEHVEMLCMGFETLEYLLRLASTPDLRRFARSALNLDVAILEPLYQLLECTGGBH | 360 |
| DB | 301 | ILEHVEMLCMGFETLEYLLRLASTPDLRRFARSALNLDVAILEPLYQLLECTGGBH | 360 |
| QY | 361 | ORGOTVSGVGVGQVLRVWRILMRIFRIKLARSHGRLAFGLTACQYQVGCILLFTAM | 420 |
| DB | 361 | ORGOTVSGVGVGQVLRVWRILMRIFRIKLARSHGRLAFGLTACQYQVGCILLFTAM | 420 |
| QY | 421 | GIFPSSAIVSYEHDPSTNFTTIPHSMMWMAVSIYGVGMYPETHLGRFAFLCIAF | 480 |
| DB | 421 | GIFPSSAIVSYEHDPSTNFTTIPHSMMWMAVSIYGVGMYPETHLGRFAFLCIAF | 480 |
| QY | 481 | GIILGMPISILYKFSYSLKAYEYTTIRREGEVNFQRAKKIAECLLSNPOLT | 540 |
| DB | 481 | GIILGMPISILYKFSYSLKAYEYTTIRREGEVNFQRAKKIAECLLSNPOLT | 540 |
| QY | 541 | PROEN 545 | |
| DB | 541 | PROEN 545 | |

Search completed: February 7, 2006, 20:47:16
Job time : 51 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 20:38:06 ; Search time 249 Seconds
(without alignments)
1544.229 Million cell updates/sec

Title: US-10-815-297-3
Perfect score: 2872
Sequence: 1 MLKOSERRSRWSYRPMWTTT.....KIIAECLGSPNQLTPROEN 545

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trcembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | DB ID | Description |
|------------|--------|-------------|--------|----------------|--------------------|
| 1 | 2872 | 100.0 | 545 | 1 KCNV2_HUMAN | Q81DN2 homo sapien |
| 2 | 2872 | 100.0 | 545 | 2 OSTRX0_HUMAN | O5T6X0 homo sapien |
| 3 | 2302.5 | 80.2 | 562 | 2 Q8CF86_MOUSE | Q8CF86 mus musculi |

ALIGNMENTS

RESULT 1
KCNV2_HUMAN STANDARD; PRT; 545 AA.
AC Q8TDN2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Potassium voltage-gated channel subfamily V member 2 (Voltage-gated
DE potassium channel subunit Kv8.2).
GN Name=KCNV2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Carchinhii; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=2205698; PubMed=12060745; DOI=10.1073/pnas.122617999;
RA Otschytsch N., Raes A., Van Hoorick D., Snyder D.J.;
RA "Oligatory heterotrimerization of three previously uncharacterized
RA Kv channel alpha-subunits identified in the human genome.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:7986-7991(2002).

CC -1- FUNCTION: Potassium channel subunit. Modulates channel activity by
CC shifting the threshold and the half-maximal activation to more
CC negative values.
CC -1- SUBUNIT: Heteromultimer with KCNB1, KCNC1 and KCNE1. Does not form
CC homomultimers.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Has to be
CC associated with KCNB1 or possibly another partner to get inserted
CC in the plasma membrane. Remains intracellular in the absence of
CC KCNB1.
CC -1- TISSUE SPECIFICITY: Detected in lung, liver, kidney, pancreas,
CC spleen, thymus, prostate, testis, ovary and colon.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the potassium channel family. V subfamily.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: AF348983; AAL83910.1; -, mRNA.
CC HSP: O27564; ILN0.
CC Ensembl: ENSG00000168263; Homo sapiens.
CC HGNC: HGNC:19698; KCNV2.
CC MIM: 607604; -.

DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003091; K channel.
DR InterPro: IPR003131; K tetra.
DR InterPro: IPR003971; Kv9 channel.
DR InterPro: IPR003968; Kv channel.
DR InterPro: IPR005820; M+channel_nlg.
DR Pfam: PF00520; Ion trans; 1.
DR Pfam: PF02214; K tetra; 1.
DR PRINTS: PR01494; K CHANNEL.
DR PRINTS: PR01494; KV9CHANNEL.
DR PRINTS: PR01494; KV9CHANNEL.

KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW Potassium; Potassium channel; Potassium transport; Transmembrane;
KW Transport; Voltage-gated channel.
FT TOPO_DOM 1 155 176 Cytoplasmic (Potential).
FT TRANSMEM 262 282 Segment S2 (Potential).
FT TRANSMEM 283 336 Cytoplasmic (Potential).
FT TOPO_DOM 337 357 Segment S3 (Potential).
FT TRANSMEM 375 395 Segment S4 (Potential).
FT TOPO_DOM 396 410 Cytoplasmic (Potential).
FT TRANSMEM 411 432 Segment S5 (Potential).
FT TRANSMEM 472 492 Segment S6 (Potential).
FT TOPO_DOM 493 545 Cytoplasmic (Potential).
FT REGION 445 465 Segment H5 (pore-forming) (Potential).
FT MOTIF 457 462 Selectivity filter (By similarity).
FT CARBOHYD 440 440 N-linked (GlcNAc...) (Potential).
SO SEQUENCE 545 AA; 62459 MW; 72D175B4C0C681DA CRC64;

Query Match 100.0%; Score 2872; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 4.7e-219;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKOSERRSRWSYRPMWTTTNGSGHRSISGLARSGQASIHMTGNTNYYIIBEDD 60
DB 1 MLKOSERRSRWSYRPMWTTTNGSGHRSISGLARSGQASIHMTGNTNYYIIBEDD 60
QY 61 GSEEDQWMDLAEBDQAGEVTTAKPEGSDPEPALSTLNVVNGHSYQDYCELAGPFX 120
DB 61 GSEEDQWMDLAEBDQAGEVTTAKPEGSDPEPALSTLNVVNGHSYQDYCELAGPFX 120
QY 121 TRLGLATSTSRQLSCDYDEQTFEDFDRDAVFLQVYVNYFLSGVLLVLDGLCPRR 180
DB 121 TRLGLATSTSRQLSCDYDEQTFEDFDRDAVFLQVYVNYFLSGVLLVLDGLCPRR 180

```
Qy 181 FLEELGYWGVRLKYYTPRCRCICEERRDELSERLKIQHELRQAQVVEAEELFRDMRFYG 240
    |||
    |||
    |||
Db 181 FLEELGYWGVRLKYYTPRCRCICEERRDELSERLKIQHELRQAQVVEAEELFRDMRFYG 240
Qy 241 PORRLNMLMEKPFSSVAKAIGVASTFVLVSVALANTVEEMQHSQGGEGPDLRP 300
    |||
    |||
    |||
Db 241 PORRLNMLMEKPFSSVAKAIGVASTFVLVSVALANTVEEMQHSQGGEGPDLRP 300
Qy 301 ILEHEVEMLCMGFFTEYLRLASTPDLRRFARSALNVDVAIPLYLQLLLECTGEGH 360
    |||
    |||
    |||
Db 301 ILEHEVEMLCMGFFTEYLRLASTPDLRRFARSALNVDVAIPLYLQLLLECTGEGH 360
Qy 361 ORGQTVSGVKGQVLRVWRMLRIFRIKLARHSTGLRPFGLTRQCYQOVGCLLFTAM 420
    |||
    |||
    |||
Db 361 ORGQTVSGVKGQVLRVWRMLRIFRIKLARHSTGLRPFGLTRQCYQOVGCLLFTAM 420
Qy 421 GFTFSAVYSVEHDVPSTNFTTIPHSMWMAVSIStVGDMYPTHGREFPFLCIAF 480
    |||
    |||
    |||
Db 421 GFTFSAVYSVEHDVPSTNFTTIPHSMWMAVSIStVGDMYPTHGREFPFLCIAF 480
Qy 481 GIILNGMPISTLYNKFSDYYSKLKAYEYTTIRREGEVNFQARAKKIAECLGSPDLT 540
    |||
    |||
    |||
Db 481 GIILNGMPISTLYNKFSDYYSKLKAYEYTTIRREGEVNFQARAKKIAECLGSPDLT 540
Qy 541 PROEN 545
    |||
    |||
    |||
Db 541 PROEN 545
```

```
RESULT 2
O5T6X0_HUMAN
ID O5T6X0_HUMAN PRELIMINARY; PRT; 545 AA.
AC O5T6X0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Potassium channel, subfamily V, member 2.
OS Homo sapiens (Human).
GN Name=KCNV2; ORFNames=RP11-526D20.3-001;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Johnson C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ354723; CA115124.1; -, Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 545 AA; 62459 MW; 72D175B4C0C6B1DA CRC64;
```

```
Query Match 100.0%; Score 2872; DB 2; Length 545;
Best local Similarity 100.0%; Pred. No. 4, 7e-219;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLCQSRRRRSWSPNNNTTNEGSHRRSICSLGARSQASGTHGTGNNVYIEEDD 60
    |||
    |||
    |||
Db 1 MLCQSRRRRSWSPNNNTTNEGSHRRSICSLGARSQASGTHGTGNNVYIEEDD 60
Qy 61 GEEEDQKDDLAEDDQAGVTTAKRGPSPDPAIISTLVNNGSHSYQUDYCELAGFPR 120
    |||
    |||
    |||
Db 61 GEEEDQKDDLAEDDQAGVTTAKRGPSPDPAIISTLVNNGSHSYQUDYCELAGFPR 120
Qy 121 TRIGRLATSTSRRLSLCDVYEQTDVEYFDRDPAPVQVLYNFYSGVLVLDGLCPRR 180
    |||
    |||
    |||
Db 121 TRIGRLATSTSRRLSLCDVYEQTDVEYFDRDPAPVQVLYNFYSGVLVLDGLCPRR 180
Qy 181 FLEELGYWGVRLKYYTPRCRCICEERRDELSERLKIQHELRQAQVVEAEELFRDMRFYG 240
```

```
Db 181 FLEELGYWGVRLKYYTPRCRCICEERRDELSERLKIQHELRQAQVVEAEELFRDMRFYG 240
    |||
    |||
    |||
Qy 241 PORRLNMLMEKPFSSVAKAIGVASTFVLVSVALANTVEEMQHSQGGEGPDLRP 300
    |||
    |||
    |||
Db 241 PORRLNMLMEKPFSSVAKAIGVASTFVLVSVALANTVEEMQHSQGGEGPDLRP 300
Qy 301 ILEHEVEMLCMGFFTEYLRLASTPDLRRFARSALNVDVAIPLYLQLLLECTGEGH 360
    |||
    |||
    |||
Db 301 ILEHEVEMLCMGFFTEYLRLASTPDLRRFARSALNVDVAIPLYLQLLLECTGEGH 360
Qy 361 ORGQTVSGVKGQVLRVWRMLRIFRIKLARHSTGLRPFGLTRQCYQOVGCLLFTAM 420
    |||
    |||
    |||
Db 361 ORGQTVSGVKGQVLRVWRMLRIFRIKLARHSTGLRPFGLTRQCYQOVGCLLFTAM 420
Qy 421 GFTFSAVYSVEHDVPSTNFTTIPHSMWMAVSIStVGDMYPTHGREFPFLCIAF 480
    |||
    |||
    |||
Db 421 GFTFSAVYSVEHDVPSTNFTTIPHSMWMAVSIStVGDMYPTHGREFPFLCIAF 480
Qy 481 GIILNGMPISTLYNKFSDYYSKLKAYEYTTIRREGEVNFQARAKKIAECLGSPDLT 540
    |||
    |||
    |||
Db 481 GIILNGMPISTLYNKFSDYYSKLKAYEYTTIRREGEVNFQARAKKIAECLGSPDLT 540
Qy 541 PROEN 545
    |||
    |||
    |||
Db 541 PROEN 545
```

```
RESULT 3
O8CF56_MOUSE
ID O8CF56_MOUSE PRELIMINARY; PRT; 562 AA.
AC O8CF56;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Potassium channel, subfamily V, member 2 (Kv11.1 modulatory voltage-
DE dependent potassium channel).
GN Name=Kcnv2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Eye;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussidi T.B., Toshynski S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Eye;
RC Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 20:41:31 ; Search time 45 Seconds
(without alignments)
1165.292 Million cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872
Sequence: 1 MLKQSERRRSWSYRPMWTE.....KKIAECLGSGNPQLPRQEN 545

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 60%
Maximum Match 100%
Listing first 500 summaries

Database : PIR 80:*

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|---------------|-------|----------------|--------|----|-------------|
| ----- | | | | | |

0 matches found

Search completed: February 7, 2006, 20:46:19
Job time : 45 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 7, 2006, 20:37:46 ; Search time 197 Seconds
(without alignments)
1215.540 Million cell updates/sec

Title: US-10-815-297-3
Perfect score: 2872
Sequence: 1 MLKOSERRSRWSYRPMNTTE.....KKIAECLGSPNQLTPROEN 545

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%
Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_21:*

| | |
|----|-----------------|
| 1: | geneeqp1980s:* |
| 2: | geneeqp1990s:* |
| 3: | geneeqp2000s:* |
| 4: | geneeqp2001s:* |
| 5: | geneeqp2002s:* |
| 6: | geneeqp2003as:* |
| 7: | geneeqp2003bs:* |
| 8: | geneeqp2004s:* |
| 9: | geneeqp2005s:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------|-------------|
| 1 | 2872 | 100.0 | 545 | AAE13610 | Human Kv1 |
| 2 | 2872 | 100.0 | 545 | ABG30991 | Human Kv1 |
| 3 | 2872 | 100.0 | 545 | AAU75091 | Novel hum |
| 4 | 2872 | 100.0 | 545 | ABP58353 | Human pot |
| 5 | 2869 | 99.9 | 545 | AAE13612 | Human Kv1 |
| 6 | 2869 | 99.9 | 545 | AAE13613 | Human Kv1 |
| 7 | 2869 | 99.9 | 545 | AAE13614 | Human Kv1 |
| 8 | 2869 | 99.9 | 545 | AAE13611 | Human Kv1 |
| 9 | 2867 | 99.8 | 545 | AAE32070 | Human TRI |
| 10 | 2865 | 99.8 | 545 | ABG79220 | Human K-a |
| 11 | 2865 | 99.8 | 545 | AAU75094 | Novel hum |
| 12 | 2862 | 99.7 | 545 | ABG79239 | Human K-a |
| 13 | 2862 | 99.7 | 545 | ABG79284 | Human K-a |
| 14 | 2857 | 99.5 | 545 | ABG79286 | Human K-a |
| 15 | 2803.5 | 97.6 | 662 | AAE22925 | Human tra |
| 16 | 2781 | 96.8 | 545 | ABG79238 | Human K-a |
| 17 | 2778 | 96.7 | 545 | ABG79285 | Human K-a |
| 18 | 2661 | 92.7 | 801 | ABBB99030 | New human |
| 19 | 2401 | 83.6 | 467 | ABU54563 | Human NOV |
| 20 | 2392.5 | 83.3 | 460 | ABM83207 | Human dia |
| 21 | 2176 | 75.8 | 416 | ABG30989 | Human vol |

ALIGNMENTS

RESULT 1
ID AAE13610 standard; protein, 545 AA.
XX
XX AAE13610;
AC
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX Human Kv10.1 protein.
DE
XX
XX Human; Kv10.1 protein; Kv10 voltage-gated potassium channel;
KW central nervous system disorder; CNS disorder; seizure disorder;
KW Parkinson's disease; migraine; psychotic disorder; schizophrenia;
KW depression; cognitive disorder; learning disorder; memory disorder;
KW neuropathic pain; vision disorder; prostate hyperplasia; stroke;
KW spermatocyte maturation; infertility; contraceptive agent;
KW neuroprotective agent; gene therapy; vaccine; epilepsy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 102..514
FT Region /note="This conserved region function as an immunogen
FT and is claimed in claim 1."
FT 472..497
FT Domain /label=S6_domain
FT
XX
XX WO200179455-A1.
XX
XX 25-OCT-2001.
XX
XX 13-APR-2001; 2001WO-US012185.
XX
XX 14-APR-2000; 2000US-0197793P.
PR 11-APR-2001; 2001US-00833466.
XX
XX (ICAGEN INC.
XX
XX Jegla TJ;
PI WPI; 2002-026021/03.
XX DR N-PSDB; AAD22817.
XX
XX Kv10.1 polypeptide for identifying potassium channel modulators,
PT comprises an alpha subunit of a Kv10 potassium channel and is capable of
PT forming a potassium channel with voltage-gating characteristics.
XX
XX Claim 16; Fig 1; 81pp; English.
PS
XX The invention relates to human Kv10.1 polypeptides and polynucleotides.
XX Kv10.1 polypeptides are members of Kv10 subfamily and Kv superfamily of
XX potassium channels. They comprise an alpha subunit of Kv10 potassium
XX channel and are capable of forming potassium channel with voltage gating
XX characteristics. They are also useful for identifying compounds that
XX increase or decrease ion flux through potassium channels. The identified
XX modulator compounds are useful for treating central nervous system (CNS)
XX disorders such as epilepsy and other seizure disorders, Parkinson's
XX disease, migraine, psychotic disorders such as schizophrenia and
XX depression, cognitive disorders such as learning and memory disorders,
XX neuropathic pain, vision disorders, prostate hyperplasia, for controlling
XX spermatocyte maturation and motility, for treating infertility, as
XX contraceptive agents and as neuroprotective agents (e.g. to prevent
XX stroke). Polynucleotides of the invention are useful in gene therapy and
XX in vaccines. The present sequence is human Kv10.1 protein
XX
XX Sequence 545 AA;
SQ
Query Match 100.0%; Score 2872; DB 5; Length 545;
Best Local Similarity 100.0%; Pred. No. 4.4e-291;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MLKOSERRRSMRYRPMWNTTNEGSHRRSICSLGARSSQASIHGTEGNVYIIEBDD 60
DB      1 MKOSERRRSMRYRPMWNTTNEGSHRRSICSLGARSSQASIHGTEGNVYIIEBDD 60
QY      61 GSEEDQWKDLAEEDQAGEVTTAKPEGSDPPALISTLNANVGSHSYOLDCELAGFPK 120
DB      61 GSEEDQWKDLAEEDQAGEVTTAKPEGSDPPALISTLNANVGSHSYOLDCELAGFPK 120
QY      121 TRLGLATSTSRSLCDYEEQDDEYFPDRPAVQLVYNFYLSGLVLDGLCPRR 180
DB      121 TRLGLATSTSRSLCDYEEQDDEYFPDRPAVQLVYNFYLSGLVLDGLCPRR 180
QY      181 FLEELGYGVRKYTPRCRCRICEERRDELSERLKIQHLELRAQAYEEAEELFRDRFYG 240
DB      181 FLEELGYGVRKYTPRCRCRICEERRDELSERLKIQHLELRAQAYEEAEELFRDRFYG 240
QY      241 PORRLNLMMEKPEFSSVAKAIGVASTVVLVVALANTVEEMQSHGQEGGPDLP 300
DB      241 PORRLNLMMEKPEFSSVAKAIGVASTVVLVVALANTVEEMQSHGQEGGPDLP 300
QY      301 ILEHVEMLCMGFPTLEYLLRLASTPDLRRFARSALNVDVAIPLPLYQLLLECFTEGH 360
DB      301 ILEHVEMLCMGFPTLEYLLRLASTPDLRRFARSALNVDVAIPLPLYQLLLECFTEGH 360
QY      361 QRGQTVGSYGKVGQVLAVRMLRIFRIILKLARHSTGLRPFGLTROCQYQVGLLFIAM 420
DB      361 QRGQTVGSYGKVGQVLAVRMLRIFRIILKLARHSTGLRPFGLTROCQYQVGLLFIAM 420
QY      421 GFTFSAAYVSEHDPSTNFTTIPSHMMAAVSISTVGYGDMYPETHLGRFPALCIAF 480
DB      421 GFTFSAAYVSEHDPSTNFTTIPSHMMAAVSISTVGYGDMYPETHLGRFPALCIAF 480
QY      481 GIILNMPISILYNKPSDYYSKLKAYEYTTIRERGEVPMQARKKIAECLLGSNPQLT 540
DB      481 GIILNMPISILYNKPSDYYSKLKAYEYTTIRERGEVPMQARKKIAECLLGSNPQLT 540
QY      541 PROEN 545
DB      541 PROEN 545

RESULT 2
ABG30991
ID      ABG30991 standard; protein; 545 AA.
AC      ABG30991;
XX      XX
DT      21-OCT-2002 (first entry)
XX      XX
DE      Human voltage gated potassium channel KV2.2.
XX      XX
KW      Voltage gated potassium channel; KV2.2; diabetes; cancer; Pick's disease;
KW      peripheral disorder; central nervous system disorder; multiple sclerosis;
KW      cardiovascular disorder; brain injury; cerebrovascular disease; stroke;
KW      Parkinson's disease; traumatic brain injury; dementia; pain;
KW      Alzheimer's disease; Huntington's disease; Creutzfeldt-Jacob dementia;
KW      schizophrenia; attention deficit disorder; spinal cord injury; epilepsy;
KW      human immunodeficiency virus; HIV; acquired immunodeficiency syndrome;
KW      AIDS; metabolic neuropathy; chronic paroxysmal hemiparesis; headache;
KW      migraine; congestive heart failure; myocardial infarction; ischaemia;
KW      arrhythmia; vascular disease; human.
XX      XX
OS      Homo sapiens.
XX      XX
PN      WO200255556-A2.
XX      XX
PD      18-JUL-2002.
XX      XX
PF      09-JAN-2002; 2002WO-EP000128.
XX      XX
PR      12-JAN-2001; 2001US-0260880P.
PR      13-NOV-2001; 2001US-0331229P.
XX      XX
```

```
PA      (FARB ) BAYER AG.
XX      XX
PI      Xiao Y;
XX      XX
DR      WPI; 2002-583653/62.
XX      XX
PT      N-PsDB; ABK89797.
XX      XX
PT      Novel human voltage gated potassium channel protein KV2.2 and
PT      polynucleotides, useful for screening modulators that are useful for
PT      treating cancer, diabetes, peripheral or central nervous system, and
XX      XX
PS      Claim 25; Fig 6; 139pp; English.
XX      XX
CC      The invention describes a purified human voltage gated potassium channel
CC      protein KV2.2 (I). (I) and the polynucleotide encoding it (II) are useful
CC      for screening for agents (III) which modify the activity of KV2.2 and
CC      (II) for detecting a polynucleotide encoding a KV2.2 in a biological
CC      sample. (III) is useful for treating a KV2.2 dysfunction related disease,
CC      such as diabetes, cancer, peripheral or central nervous system (CNS)
CC      disorders, or cardiovascular disorders. The CNS disorders treatable
CC      include brain injuries, cerebrovascular diseases, Parkinson's disease,
CC      multiple sclerosis, traumatic brain injury, stroke, dementia, Alzheimer's
CC      disease, vascular dementia, Parkinsonism linked to chromosome 17, Pick's
CC      disease, Huntington's disease, Creutzfeldt-Jacob dementia, schizophrenia
CC      with dementia, attention deficit disorders, spinal cord injury, traumatic brain
CC      injuries, epilepsy, human immunodeficiency virus (HIV)/acquired
CC      immunodeficiency syndrome (AIDS) related pain, cancer pain, metabolic
CC      neuropathies, headache pain (e.g. migraine), chronic paroxysmal
CC      hemiparesis and tension-type like headache. Cardiovascular diseases
CC      treatable include congestive heart failure, myocardial infarction,
CC      ischaemic disease of the heart, all kinds of atrial and ventricular
CC      arrhythmias, hypertensive and peripheral vascular diseases. This is the
CC      amino acid sequence of human voltage gated potassium channel KV2.2
XX      XX
SQ      Sequence 545 AA;
XX      XX
Query Match      100.0%; Score 2872; DB 5; Length 545;
Best Local Similarity 100.0%; Pred. No. 4,4e-291;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MLKOSERRRSMRYRPMWNTTNEGSHRRSICSLGARSSQASIHGTEGNVYIIEBDD 60
DB      1 MKOSERRRSMRYRPMWNTTNEGSHRRSICSLGARSSQASIHGTEGNVYIIEBDD 60
QY      61 GSEEDQWKDLAEEDQAGEVTTAKPEGSDPPALISTLNANVGSHSYOLDCELAGFPK 120
DB      61 GSEEDQWKDLAEEDQAGEVTTAKPEGSDPPALISTLNANVGSHSYOLDCELAGFPK 120
QY      121 TRLGLATSTSRSLCDYEEQDDEYFPDRPAVQLVYNFYLSGLVLDGLCPRR 180
DB      121 TRLGLATSTSRSLCDYEEQDDEYFPDRPAVQLVYNFYLSGLVLDGLCPRR 180
QY      181 FLEELGYGVRKYTPRCRCRICEERRDELSERLKIQHLELRAQAYEEAEELFRDRFYG 240
DB      181 FLEELGYGVRKYTPRCRCRICEERRDELSERLKIQHLELRAQAYEEAEELFRDRFYG 240
QY      241 PORRLNLMMEKPEFSSVAKAIGVASTVVLVVALANTVEEMQSHGQEGGPDLP 300
DB      241 PORRLNLMMEKPEFSSVAKAIGVASTVVLVVALANTVEEMQSHGQEGGPDLP 300
QY      301 ILEHVEMLCMGFPTLEYLLRLASTPDLRRFARSALNVDVAIPLPLYQLLLECFTEGH 360
DB      301 ILEHVEMLCMGFPTLEYLLRLASTPDLRRFARSALNVDVAIPLPLYQLLLECFTEGH 360
QY      361 QRGQTVGSYGKVGQVLAVRMLRIFRIILKLARHSTGLRPFGLTROCQYQVGLLFIAM 420
DB      361 QRGQTVGSYGKVGQVLAVRMLRIFRIILKLARHSTGLRPFGLTROCQYQVGLLFIAM 420
QY      421 GFTFSAAYVSEHDPSTNFTTIPSHMMAAVSISTVGYGDMYPETHLGRFPALCIAF 480
DB      421 GFTFSAAYVSEHDPSTNFTTIPSHMMAAVSISTVGYGDMYPETHLGRFPALCIAF 480
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